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Q9S1T9          PRELIMINARY:      PRT:      215 AA.
ID  Q9S1T9
AC  Q9S1T9
DE  01-MAY-2000 (TEMBLrel. 13, Created)
DT  01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE  01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE  POTATIVE CCAAT-BOX BINDING TRANSCRIPTION FACTOR.
GN  ATG13570.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC  Magnoliophyta: eudicotyledons: core eudicots: kosisids 11.
OC  Brassicales: Brassicaceae: Arabidopsis.
OX  NBL_TaxID: 3702.
RN  11
RP  SEQUENCE FROM N.A.
RC  STRAIN=CV. COLUMBIA;
RX  MEDLINE=20083467; PubMed=1661197;
RA  Lin X., Kaul S., Kounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA  Fujii C.Y., Mason T.M., Bowman G.T., Barnstead M.P., Feldberg T.V.,
RA  Buell C.R., Ketchum K.A., Lee J.L., Ponting C.M., Koo H., Moffat K.S.,
RA  Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon J., Gill J.E.,
RA  Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA  Copchaver G.P., Prouss D., Newman W.C., White O., Eisen J.A.,
RA  Salzberg S.L., Fraser C.M., Venter J.C.,
RT  Sequence and analysis of chromosome 11 of Arabidopsis thaliana.
RI  Nature 402:761-766(1999).
DR  FMBL: AC007063; AAD2680.1; -.
DR  HSSP: P48781; 1B67.
DR  InterPro: IPR000166; -.
DR  InterPro: IPR000947; -.
DR  Pfam: PF00808; CHFD_NFYB_HMP; 1.
DR  PRINTS: PR00615; CCAATSUBNTA.
DR  PROSITE: PS00685; CCAAT_NFYB; 1.
SQ  SEQUENCE 215 AA; 24619 MW; 0615B267A977D25 CRC64;

Query Match          41.8%; Score 336; DB 10; Length 215,
Best Local Similarity 61.5%; Pred. No. 4.5e-25;
Matches 59; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

QY  1 REDDITLAWNSKIRINMKTLPSHAKISDIAKFTIQVSVSYISFTVGEANFPGQPPPT 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  45 KPDPEPIANVAVIKMKVAVPQVYVAVKAVYCYKYPTEDEK 130
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  61 ITADITLWMSKIRFNVYDITVFINPPTFGSALPGEPSTLQVYQNCIGPHG 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  95 INEDITLWMSKIRFNVYDITVFINPPTFGSALPGEPSTLQVYQNCIGPHG 130
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q00735          PRELIMINARY:      PRT:      186 AA.
ID  Q00735
AC  Q00735
DE  01-NOV-1996 (TEMBLrel. 01, Created)
DT  01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DE  01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE  PUTATIVE COMPONENT OF CCAAT BINDING COMPLEX HAPC.
GN  HAPC.
OS  Emerizella nidulans (Aspergillus nidulans).
OC  Eukaryota: Fungi: Ascomycota: Pezizomycotina: Emericellales:
OC  Eurotiiales: Trichocomaceae: Emericella.
OX  NBL_TaxID 5072;
RN  11
RP  SEQUENCE FROM N.A.
RC  MEDLINE=95147853; PubMed 745362;
RA  Mulder N., Scholten J.H., de Boer R.W., Grievell L.A.;
RT  Sequence of the HAPC transcription factor of Kluyveromyces fragilis
RT  predicts the presence of a novel 4-cysteine zinc-finger motif.
RI  Mol. Gen. Genet. 245:96-106(1994).
RN  12
RP  SEQUENCE FROM N.A.
RC  MEDLINE=96285564; PubMed 8709944;
RA  Papadimitrakopoulos F., Andrianopoulos A., Sharif J.A., Davis M.A.

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RA  Hynes M.J.;
RT  "The hapt gene of Aspergillus nidulans is involved in the expression
RT  of CCAAT-containing promoters.";
RI  Mol. Gen. Genet. 251:412-421(1996).
DR  EMBL: U35341; AAC49411.1; -.
DR  HSSP: P48781; 1B67.
DR  InterPro: IPR000166; -.
DR  InterPro: IPR000947; -.
DR  Pfam: PF00808; CHFD_NFYB_HMP; 1.
DR  PRINTS: PR00615; CCAATSUBNTA.
DR  PROSITE: PS00685; CCAAT_NFYB; 1.
SQ  SEQUENCE 186 AA; 20616 MW; 2FCFDD50F0B0B03D CRC64;

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Query Match          41.0%; Score 330; DB 3; Length 186;
Best Local Similarity 50.0%; Pred. No. 1.5e-24;
Matches 63; Conservative 29; Mismatches 26; Indels 8; Gaps 2;

QY  1 EFQGGYMIITAVIRIKMKTLPSHAKISDIAKFTIQVSVSYISFTVGEANFPGQPPPT 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  42 KPDPEPIANVAVIKMKVAVPQVYVAVKAVYCYKYPTEDEK 101
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  61 ITADITLWMSKIRFNVYDITVFINPPTFGSALPGEPSTLQVYQNCIGPHG 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  102 VNGEDITLWMSKIRFNVYDITVFINPPTFGSALPGEPSTLQVYQNCIGPHG 153
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  121 PSKGLP 126
    :|||
DB  154 PSKGLP 159
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RESULT 13
Q37744          PRELIMINARY:      PRT:      206 AA.
ID  Q37744
AC  Q37744
DE  01-AUG-1998 (TEMBLrel. 07, Created)
DT  01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DE  01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE  NUCLEAR Y/CCAAT BOX BINDING FACTOR B SUBUNIT N-YB.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC  Amphibia: Batrachia: Anura; Mesobatrachia: Pipridae: Pipidae;
OC  Xenopodinae: Xenopus.
OX  NBL_TaxID=8355;
RN  11
RP  SEQUENCE FROM N.A.
RC  Submited (JAN-1998) to the FMB/GenBank/EMBL databases.
RA  Herlihy M., Wolfe A.P.;
DR  EMBL: AF041204; AAC82336.1; -.
DR  HSSP: P48781; 1B67.
DR  InterPro: IPR000166; -.
DR  InterPro: IPR000947; -.
DR  Pfam: PF00808; CHFD_NFYB_HMP; 1.
DR  PRINTS: PR00615; CCAATSUBNTA.
DR  PROSITE: PS00685; CCAAT_NFYB; 1.
SQ  SEQUENCE 206 AA; 22582 MW; 359373B2VAF41667 CRC64;

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Query Match          40.9%; Score 328.5; DB 13; Length 206;
Best Local Similarity 53.8%; Pred. No. 2.3e-24;
Matches 63; Conservative 23; Mismatches 24; Indels 7; Gaps 1;

QY  1 REDDITLWNSKIRINMKTLPSHAKISDIAKFTIQVSVSYISFTVGEANFPGQPPPT 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  52 KPDPEPIANVAVIKMKVAVPQVYVAVKAVYCYKYPTEDEK 111
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  61 ITADITLWMSKIRFNVYDITVFINPPTFGSALPGEPSTLQVYQNCIGPHG 117
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB  112 INEDITLWMSKIRFNVYDITVFINPPTFGSALPGEPSTLQVYQNCIGPHG 161
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 14
Q59848

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